from blood cultures, *C. parapsilosis* and *C. tropicalis* were detected up to ten fold more often in comparison to other sources of isolation. This difference in local epidemiology should be taken into account for treatment decisions of candidemia.

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Differential Expression Study of a Potentially Novel Gene in *Candida albicans* Morphology Switching

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Candidiasis and systemic candidiasis are on the rise in recent years, especially in immunologically challenged persons. Morphology switching in *Candida albicans*, the most virulent human fungal pathogen, has been identified as one important factor of virulence. Nevertheless, the exact mechanism of this phenomenon has not been fully understood. This has prompted intensive research into the genetic aspects of *Candida albicans* pathogenicity, albeit the elusive gene(s) causing morphology switching has not been uncovered. In our study, an uncharacterized gene fragment of interest was previously found via differential display reverse transcription-PCR. A1—1 was identified as upregulated in the *Candida albicans* hyphal forms at 1, 3 and 6 hours after hyphal induction compared to the yeast form. The differential expression of A1—1 in yeast-hyphae switching was then studied in further detail. *Candida albicans* yeast forms were grown at 25 °C in Winge medium. Half of this culture was incubated in hyphal-induction conditions in RPMI-1640 added with penicillin-streptomycin and fetal bovine serum at 37 °C with 5% CO_2. RNA from the yeast form and hyphal forms at 1, 3, 6, 12 and 24 hour time-points were extracted. All RNA were reverse transcribed into cDNA. A1—1 sequence-specific primers were designed, with beta-actin as the housekeeping gene. The Pfaffl mathematical method of relative quantitative real-time PCR using SYBR Green was used to validate the differential expression. A1—1 was found to be upregulated in the hyphal forms of *Candida albicans*. This gene fragment has presented itself as an interesting target for ongoing further studies to elucidate the function of this potentially novel gene in *Candida albicans* yeast-hyphae morphology switching.

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Prevalence of *Trichophyton rubrum* in Tehran, Isolated from Different Levels of Society and Study of Its Probable Organ Orientation

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Background: Trichophyton rubrum is the most common dermatophyte species and the most frequent cause of fungal skin infections in humans worldwide. It's a major concern because feet and nail infections caused by this organism is extremely difficult to cure.

Methods: A total of 3942 patients referred to Mycology Department of Pasteur Institute of Iran, were examined for fungal infection during 20march 2006 to 20march 2007. Samples were gathered by scalping the suspected area, and then were inspected by microscope and also were cultured. Two different media (Sabouro-Dextrose-Agar with Choloramphenicol and Sabouro-Dextrose-Agar with Choloramphenicol and Cyclohexamid) were used for all samples to specify the name of fungus in positive ones and also to confirm lack of them in negative samples.

Results: The proportion of male and female in number of people who were examined for fungal infections was equal. % 5.63 of whole (222 people) suffered from *Trichophyton rubrum* infection that %63.5 of them were men. People between 41 to 50 years old were the most infected by this fungus, followed by age groups of 31—40, 21—30, 51—60 and 10—20 years old respectively. There were just a few people in 61—70 and 71—80 years old groups infected and only one child under 10 years old was infected by *Trichophyton rubrum*. Totally sole was the most involved organ followed by groin, toe webs and sole together, toe nail, toe webs singly and foot. However *Trichophyton rubrum* trended to infect men's groins slightly more than their soles.

Conclusion: There should be more care about hygienic issues especially for people who are in their active age and are unavoidably involved in social activities. It is recommended not to use common wears especially shoes and slippers in order to decline the rate of *Trichophyton rubrum* infection.

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45.034

Molecular Differentiation and Antifungal Susceptibility of *Candida parapsilosis* Isolated from Patients with Fungemia

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The genetic heterogeneity and antifungal susceptibility patterns of *Candida parapsilosis* isolated from blood cultures of our patients were examined in this study. Polymerase chain reaction of yeast DNA with a single primer generated four unique fingerprints for the 45 blood isolates investigated in this study. Based on the fingerprints, the isolates were identified as genotype P1 (32 isolates), P2 (10 isolates), P3 (2 isolates) and P4 (1 isolate). Sequence analysis

of the ITS region of the isolates identified genotype P1 as *C. parapsilosis*, genotype P2 as *C. orthopsilosis*, genotype P3 as *C. metapsilosis* and genotype P4 as *Lodderomyces elongisporus*. Antifungal susceptibility testing using Etest showed that all isolates tested were susceptible to amphotericin B, fluconazole, ketoconazole, itraconazole and voriconazole. Although *C. parapsilosis* isolates exhibited higher MIC_{50}s than those of *C. orthopsilosis* for all the drugs tested, no significant difference in the MICs for both *Candida* species was observed.

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45.035

Epidemiological Study of Cryptococcosis in Malaysia

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This paper described the isolation of *Cryptococcus neoformans* and *C. gattii* from patients with chronic meningitis who attended to Malaysian hospitals, from 2003 to 2004. Of 96 cryptococcal cases reported for the two-year period, 74 (77.1%) were male and 40 (41.7%) patients were between 31—40 years old. A total of 57 (59.4%) and 23 (24.0%) patients were Malay and Chinese, respectively. HIV infections are the major underlying diseases which were reported in 38 (39.6%) patients. *C. neoformans* was the predominant *Cryptococcus* species isolated from 88.5% of cryptococcal cases in this country. Cryptococcal cases due to *C. neoformans* (all were serotype A and molecular type VNI) were reported from all the regions in Malaysia with the most number of cases observed in the Central and Northern regions. *C. gattii* (all were serotype B and molecular types VGI/II) were isolated from all the regions except for the Southern region. Comparing to a previous study conducted prior to AIDS era, there were substantial changes in the demographic characteristics of patient population and type of *Cryptococcus* spp. isolated in this study.

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45.036

Mycetoma and Its Varied Presentations - A Study of 11 Cases

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Introduction: Mycetoma is a chronic granulomatous infection that is present worldwide and endemic in tropical and subtropical regions. Mycetoma may be caused by various species of fungi (eumycetoma) or bacterial (actinomycetoma) which occur as saprophytes in soil or on plants. From these sources, they are implanted subcutaneously, usually after a penetrating injury among agricultural workers. Adult males are therefore most often infected. It generally remains localized causing cutaneous and subcutaneous tissue swelling, nodule formation, and discharging sinuses. Grains are discharged onto the skin surface via these sinuses.

Material and methods: It is a retrospective study consisting of 11 cases of mycetoma that presented to Kasturba Medical College Hospital, Manipal, Karnataka, India during a period 4 years from 2004 to 2007. All the cases were categorized depending upon the age, sex, duration of onset, site of involvement, radiological features, histopathology and culture.

Results: In our study, out of 11 patients, 10 cases were caused by bacteria (Actinomycetoma) and one was caused by fungus (Eumycetoma). Majority of patients were males (8 cases). Most common site of involvement was foot in 10 cases and hand in one case. Duration of disease was ranging from 8 months to 10 years. All the cases improved with medical treatment except for two cases where surgical debulking was done along with medical treatment. Most commonly used drug was Dapsone and cotrimoxazole along with Inj. Streptomycin or Cap. Rifampicin. Two cases with recurrence were treated with modified Welsh regimen. Eumycotic case was treated with Ketoconazole.

Conclusion: Most common cause of Madura foot is Actinomyces and Nocardia. If diagnosed early and treated appropriately, we can expect a favorable outcome.

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45.037

Feline Sporotrichosis - Transmission to Man? A Case Report

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Introduction: Sporotrichosis is an indolent fungal infection of humans and animals caused by Sporothrix schenkii. Feline sporotrichosis is a rare disease but has significant zoonotic potential. Transmission to humans occurs from handling of diseased cat or its infected bedding or by direct inoculation.

Case Report: A 62 year old male, a native of Kudremukh, presented with symptomatic nodular swellings over right forearm of two months duration which he attributed to flea bite from a cat. Cutaneous examination revealed presence of three firm, mobile, non tender nodular lesions over right elbow. He was treated with topical steroids after considering a provisional diagnosis of foreign body granuloma. He presented three months later with development of multiple noduloulcerative lesions in a linear distribution along the right forearm and arm. Meanwhile his cat had also developed similar lesions, became sick and died. PAS stained histopathology section of lesion showed scattered spores and a granulomatous reaction. Fungal culture demonstrated growth of *Sporothrix schenckii* and mould form was demonstrated by Calcofluor white mount preparation. He showed dramatic improvement with resolution of lesions in four weeks following treatment with oral saturated potassium iodide solution.

Discussion: The largest collection of cases of feline sporotrichosis has been reported from Brazil and isolated reports exist in North American literature. However no mention exists in Indian literature. Our patient presented with history and clinical findings suggestive of feline acquired lymphocutaneous sporotrichosis. Culture and histopathology findings corroborated with this and he